



0590 04D0  
02/12/02

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/045,400  
Source: OIPR  
Date Processed by STIC: 2/5/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**Raw Sequence Listing Error Summary**

**ERROR DETECTED**

**SUGGESTED CORRECTION**

**SERIAL NUMBER: 10/045,400**

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence

11  Use of <220>  
-      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n  
-      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002  
TIME: 17:06:00

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02052002\J045400.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Moon, Chulso  
4 Mao, Li  
6 <120> TITLE OF INVENTION: Dap-Kinase and Hoxa9, Two Human Genes Associated With  
Genesis,

7 Progression, and Aggressiveness of Non-Small Cell Lung Cancer

9 <130> FILE REFERENCE: 10620-1U1

11 <140> CURRENT APPLICATION NUMBER: US/10/045,400

12 <141> CURRENT FILING DATE: 2001-11-29

14 <150> PRIOR APPLICATION NUMBER: US 60/250,083

15 <151> PRIOR FILING DATE: 2000-11-29

17 <160> NUMBER OF SEQ ID NOS: 7

19 <170> SOFTWARE: PatentIn version 3.0

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 20

23 <212> TYPE: DNA

C--> 24 <213> ORGANISM: Artificial/Unknown

invalid - see item 10 on Error Summary  
Sheet

26 <220> FEATURE:

27 <221> NAME/KEY: misc\_feature

28 <222> LOCATION: (1)..(20)

29 <223> OTHER INFORMATION: HoxA9 PCR Primer

32 <400> SEQUENCE: 1

20

33 ccggccttat ggcattaaac

36 <210> SEQ ID NO: 2

37 <211> LENGTH: 20

38 <212> TYPE: DNA

C--> 39 <213> ORGANISM: Artificial/Unknown

41 <220> FEATURE:

42 <221> NAME/KEY: misc\_feature

43 <222> LOCATION: (1)..(20)

44 <223> OTHER INFORMATION: HoxA9 PCR Primer

47 <400> SEQUENCE: 2

20

48 agttggctgc tgggttattg

51 <210> SEQ ID NO: 3

52 <211> LENGTH: 218

53 <212> TYPE: DNA

C--> 54 <213> ORGANISM: Artificial/Unknown

56 <220> FEATURE:

57 <221> NAME/KEY: misc\_feature

58 <222> LOCATION: (1)..(218)

59 <223> OTHER INFORMATION: HOXA9 Probe

62 <400> SEQUENCE: 3

63 ccggccttat ggcattaaac ctgaaccgct gtcggccaga aggggtgact gtccccacgct

60

65 tgacactcac actttgtccc tgactgacta tgcttgggt ttcctccag ttgatagaga

120

67 aaaacaaccc agcgaaggcg ccttctccga aaacaatgcc gagaatgaga gcggcggaga

180

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002  
TIME: 17:06:00

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Output Set: N:\CRF3\02052002\J045400.raw

69	caagcccccc atcgatccca ataaccaggc agccaa	218
72	<210> SEQ ID NO: 4	
73	<211> LENGTH: 5910	
74	<212> TYPE: DNA	
75	<213> ORGANISM: Homo sapiens	
77	<220> FEATURE:	
78	<221> NAME/KEY: CDS	
79	<222> LOCATION: (337)..(4632)	
81	<400> SEQUENCE: 4	
82	cgaggacag ccggaccgag ccaacgcgg ggactttgtt ccctccacgg agggactcg	60
84	gcaactcgca gcgccagggt ctggggccgg cgcctggag ggatctgcgc ccccaactca	120
86	ctccctagct gtgttcccgcc cgccgcggc gctagtcgc ggcgcgtggcg cctatggcg	180
88	gcctccgaca gcgctccggc gggaccgggg gagctcccgag ggcgcgggca ctggagactg	240
90	atgcatgagg ggcctacggc ggcgcaggag cggtgtgtat ggtctggaa gcgagactga	300
92	agtccctgg gcttttgtga ggcgtgacag ttatc atg acc gtg ttc agg cag	354
93	Met Thr Val Phe Arg Gln	
94	1 5	
96	gaa aac gtg gat gat tac tac gac acc ggc gag gaa ctt ggc agt gga	402
97	Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly	
98	10 15 20	
100	cag ttt gcg gtt gtg aag aaa tgc cgt gag aaa agt acc ggc ctc cag	450
101	Gln Phe Ala Val Val Lys Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln	
102	25 30 35	
104	tat gcc gcc aaa ttc atc aag aaa agg agg act aag tcc agc cgg cgg	498
105	Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg	
106	40 45 50	
108	ggt gtg agc cgc gag gac atc gag cgg gag gtc agc atc ctg aag gag	546
109	Gly Val Ser Arg Glu Asp Ile Glu Arg Glu Val Ser Ile Leu Lys Glu	
110	55 60 65 70	
112	atc cag cac ccc aat gtc atc acc ctg cac gag gtc tat gag aac aag	594
113	Ile Gln His Pro Asn Val Ile Thr Leu His Glu Val Tyr Glu Asn Lys	
114	75 80 85	
116	acg gac gtc atc ctg atc ttg gaa ctc gtt gca ggt ggc gag ctg ttt	642
117	Thr Asp Val Ile Leu Ile Leu Glu Leu Val Ala Gly Gly Glu Leu Phe	
118	90 95 100	
120	gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa	690
121	Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr Glu Glu Ala Thr Glu	
122	105 110 115	
124	ttt ctc aaa caa att ctt aat ggt gtt tac tac ctg cac tcc ctt caa	738
125	Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr Tyr Leu His Ser Leu Gln	
126	120 125 130	
128	atc gcc cac ttt gat ctt aag cct gag aac ata atg ctt ttg gat aga	786
129	Ile Ala His Phe Asp Leu Lys Pro Glu Asn Ile Met Leu Leu Asp Arg	
130	135 140 145 150	
132	aat gtc ccc aaa cct cgg atc aag atc att gac ttt ggg ttg gcc cat	834
133	Asn Val Pro Lys Pro Arg Ile Lys Ile Ile Asp Phe Gly Leu Ala His	
134	155 160 165	
136	aaa att gac ttt gga aat gaa ttt aaa aac atg ttt ggg act cca gag	882
137	Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu	

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138	170	175	180	
140	ttt gtc gct cct gag ata gtc aac tat gaa cct ctt ggt ctt gag gca			930
141	Phe Val Ala Pro Glu Ile Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala			
142	185	190	195	
144	gat atg tgg agt atc ggg gta ata acc tat atc ctc cta agt ggg gcc			978
145	Asp Met Trp Ser Ile Gly Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala			
146	200	205	210	
148	tcc cca ttt ctt gga gac act aag caa gaa acg tta gca aat gta tcc			1026
149	Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Val Ser			
150	215	220	225	230
152	gct gtc aac tac gaa ttt gag gat gaa tac ttc agt aat acc agt gcc			1074
153	Ala Val Asn Tyr Glu Phe Asp Glu Tyr Phe Ser Asn Thr Ser Ala			
154	235	240	245	
156	cta gcc aaa gat ttc ata aga aga ctt ctg gtc aag gat cca aag aag			1122
157	Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu Val Lys Asp Pro Lys Lys			
158	250	255	260	
160	aga atg aca att caa gat agt ttg cag cat ccc tgg atc aag cct aaa			1170
161	Arg Met Thr Ile Gln Asp Ser Leu Gln His Pro Trp Ile Lys Pro Lys			
162	265	270	275	
164	gat aca caa cag gca ctt agt aga aaa gca tca gca gta aac atg gag			1218
165	Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala Ser Ala Val Asn Met Glu			
166	280	285	290	
168	aaa ttc aag aag ttt gca gcc cgg aaa aaa tgg aaa caa tcc gtt cgc			1266
169	Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys Trp Lys Gln Ser Val Arg			
170	295	300	305	310
172	ttg ata tca ctg tgc caa aga tta tcc agg tca ttc ctg tcc aga agt			1314
173	Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg Ser Phe Leu Ser Arg Ser			
174	315	320	325	
176	aac atg agt gtt gcc aga agc gat gat act ctg gat gag gaa gac tcc			1362
177	Asn Met Ser Val Ala Arg Ser Asp Asp Thr Leu Asp Glu Asp Ser			
178	330	335	340	
180	ttt gtg atg aaa gcc atc atc cat gcc atc aac gat gac aat gtc cca			1410
181	Phe Val Met Lys Ala Ile Ile His Ala Ile Asn Asp Asp Asn Val Pro			
182	345	350	355	
184	ggc ctg cag cac ctt ctg ggc tca tta tcc aac tat gat gtt aac caa			1458
185	Gly Leu Gln His Leu Leu Gly Ser Leu Ser Asn Tyr Asp Val Asn Gln			
186	360	365	370	
188	ccc aac aag cac ggg aca cct cca tta ctc att gct gct ggc tgt ggg			1506
189	Pro Asn Lys His Gly Thr Pro Pro Leu Leu Ile Ala Ala Gly Cys Gly			
190	375	380	385	390
192	aat att caa ata cta cag ttg ctc att aaa aga ggc tcg aga atc gat			1554
193	Asn Ile Gln Ile Leu Gln Leu Ile Lys Arg Gly Ser Arg Ile Asp			
194	395	400	405	
196	gtc cag gat aag ggc ggg tcc aat gcc gtc tac tgg gct gct cgg cat			1602
197	Val Gln Asp Lys Gly Ser Asn Ala Val Tyr Trp Ala Ala Arg His			
198	410	415	420	
200	ggc cac gtc gat acc ttg aaa ttt ctc agt gag aac aaa tgc cct ttg			1650
201	Gly His Val Asp Thr Leu Lys Phe Leu Ser Glu Asn Lys Cys Pro Leu			
202	425	430	435	

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204 gat gtg aaa gac aag tct gga gag atg gcc ctc cac gtg gca gct cgc	1698
205 Asp Val Lys Asp Lys Ser Gly Glu Met Ala Leu His Val Ala Ala Arg	
206 440 445 450	
208 tat ggc cat gct gac gtg gct caa gtt act tgt gca gct tcg gct caa	1746
209 Tyr Gly His Ala Asp Val Ala Gln Val Thr Cys Ala Ala Ser Ala Gln	
210 455 460 465 470	
212 atc cca ata tcc agg aca aag gaa gaa acc ccc ctg cac tgt gct	1794
213 Ile Pro Ile Ser Arg Thr Lys Glu Glu Thr Pro Leu His Cys Ala	
214 475 480 485	
216 gct tgg cac ggc tat tac tct gtg gcc aaa gcc ctt tgt gaa gcc ggc	1842
217 Ala Trp His Gly Tyr Ser Val Ala Lys Ala Leu Cys Glu Ala Gly	
218 490 495 500	
220 tgt aac gtg aac atc aag aac cga gaa gga gag acg ccc ctc ctg aca	1890
221 Cys Asn Val Asn Ile Lys Asn Arg Glu Gly Glu Thr Pro Leu Leu Thr	
222 505 510 515	
224 gcc tct gcc agg ggc tac cac gac atc gtg gag tgt ctg gcc gaa cat	1938
225 Ala Ser Ala Arg Gly Tyr His Asp Ile Val Glu Cys Leu Ala Glu His	
226 520 525 530	
228 gga gcc gac ctt aat gct tgc gac aag gac gga cac att gcc ctt cat	1986
229 Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp Gly His Ile Ala Leu His	
230 535 540 545 550	
232 ctg gct gta aga cgg tgt cag atg gag gta atc aag act ctc ctc agc	2034
233 Leu Ala Val Arg Arg Cys Gln Met Glu Val Ile Lys Thr Leu Leu Ser	
234 555 560 565	
236 caa ggg tgt ttc gtc gat tat caa gac agg cac ggc aat act ccc ctc	2082
237 Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg His Gly Asn Thr Pro Leu	
238 570 575 580	
240 cat gtg gca tgt aaa gat ggc aac atg cct atc gtg gtg gcc ctc tgt	2130
241 His Val Ala Cys Lys Asp Gly Asn Met Pro Ile Val Val Ala Leu Cys	
242 585 590 595	
244 gaa gca aac tgc aat ttg gac atc tcc aac aag tat ggg cga acg cct	2178
245 Glu Ala Asn Cys Asn Leu Asp Ile Ser Asn Lys Tyr Gly Arg Thr Pro	
246 600 605 610	
248 ctg cac ctt ggc aac aac gga atc cta gac gtg gtc cgg tat ctc	2226
249 Leu His Leu Ala Ala Asn Asn Gly Ile Leu Asp Val Val Arg Tyr Leu	
250 615 620 625 630	
252 tgt ctg atg gga gcc agc gtt gag gcg ctg acc acg gac gga aag acg	2274
253 Cys Leu Met Gly Ala Ser Val Glu Ala Leu Thr Thr Asp Gly Lys Thr	
254 635 640 645	
256 gca gaa gat ctt gct aga tcg gaa cag cac gag cac gta gca ggt ctc	2322
257 Ala Glu Asp Leu Ala Arg Ser Glu Gln His Glu His Val Ala Gly Leu	
258 650 655 660	
260 ctt gca aga ctt cga aag gat acg cac cga gga ctc ttc atc cag cag	2370
261 Leu Ala Arg Leu Arg Lys Asp Thr His Arg Gly Leu Phe Ile Gln Gln	
262 665 670 675	
264 ctc cga ccc aca cag aac ctg cag cca aga att aag ctc aag ctg ttt	2418
265 Leu Arg Pro Thr Gln Asn Leu Gln Pro Arg Ile Lys Leu Lys Leu Phe	
266 680 685 690	
268 ggc cac tcg gga tcc ggg aaa acc acc ott gta gaa tct ctc aag tgt	2466

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Input Set : A:\ES.txt  
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269	Gly	His	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Val	Glu	Ser	Leu	Lys	Cys	
270	695							700				705				710	
272	ggg	ctg	ctg	agg	agc	ttt	ttc	aga	agg	cgt	cg	ccc	aga	ctg	tct	tcc	2514
273	Gly	Leu	Leu	Arg	Ser	Phe	Phe	Arg	Arg	Arg	Arg	Arg	Pro	Arg	Leu	Ser	Ser
274								715				720				725	
276	acc	aac	tcc	agc	agg	ttc	cca	cct	tca	ccc	ctg	gct	tct	aag	ccc	aca	2562
277	Thr	Asn	Ser	Ser	Arg	Phe	Pro	Pro	Ser	Pro	Leu	Ala	Ser	Lys	Pro	Thr	
278								730				735				740	
280	gtc	tca	gtg	agc	atc	aac	ctg	tac	cca	ggc	tgc	gag	aac	gtg	agt		2610
281	Val	Ser	Val	Ser	Ile	Asn	Asn	Leu	Tyr	Pro	Gly	Cys	Glu	Asn	Val	Ser	
282								745				750				755	
284	gtg	agg	agc	cgc	agc	atg	atg	ttc	gag	ccg	gg	ctt	acc	aaa	ggg	atg	2658
285	Val	Arg	Ser	Arg	Ser	Met	Met	Phe	Glu	Pro	Gly	Leu	Thr	Lys	Gly	Met	
286								760				765				770	
288	ctg	gag	gtg	ttt	gtg	gcc	ccg	acc	cac	cac	ccg	acc	tgc	tgc	gcc	gat	2706
289	Leu	Glu	Val	Phe	Val	Ala	Pro	Thr	His	His	Pro	His	Cys	Ser	Ala	Asp	
290								775				780				785	
292	gac	cag	tcc	acc	aag	goc	atc	gac	atc	cag	aac	gct	tat	ttg	aat	gga	2754
293	Asp	Gln	Ser	Thr	Lys	Ala	Ile	Asp	Ile	Gln	Asn	Ala	Tyr	Leu	Asn	Gly	
294								795				800				805	
296	gtt	ggc	gat	ttc	agc	gtg	tgg	gag	ttc	tct	gga	aat	cct	gtg	tat	ttc	2802
297	Val	Gly	Asp	Ser	Val	Trp	Glu	Phe	Ser	Gly	Asn	Pro	Val	Tyr	Phe		
298								810				815				820	
300	tgc	tgt	tat	gac	tat	ttt	gct	gca	aat	gat	ccc	acg	tca	atc	cat	gtt	2850
301	Cys	Cys	Tyr	Asp	Tyr	Phe	Ala	Ala	Asn	Asp	Pro	Thr	Ser	Ile	His	Val	
302								825				830				835	
304	gtt	gtc	ttt	agt	cta	gaa	gag	ccc	tat	gag	atc	cag	ctg	aac	cca	gtg	2898
305	Val	Val	Phe	Ser	Leu	Glu	Glu	Pro	Tyr	Glu	Ile	Gln	Leu	Asn	Pro	Val	
306								840				845				850	
308	att	ttc	tgg	ctc	agt	ttc	ctg	aag	tcc	ctt	gtc	gaa	gaa	ggc	gag		2946
309	Ile	Phe	Trp	Leu	Ser	Phe	Leu	Lys	Ser	Leu	Val	Pro	Val	Glu	Glu	Pro	
310								855				860				865	
312	ata	gcc	tcc	ggt	ggc	aag	ctg	aag	aac	cca	ctc	caa	gtt	gtc	ctg	gtg	2994
313	Ile	Ala	Phe	Gly	Gly	Lys	Leu	Lys	Asn	Pro	Leu	Gln	Val	Val	Leu	Val	
314								875				880				885	
316	gcc	acc	cac	gct	gac	atc	atg	aat	gtt	cct	cga	ccg	gct	gga	ggc	gag	3042
317	Ala	Thr	His	Ala	Asp	Ile	Met	Asn	Val	Pro	Arg	Pro	Ala	Gly	Gly	Glu	
318								890				895				900	
320	ttt	gga	tat	gac	aaa	gac	aca	tcg	tgg	ctg	aaa	gag	att	agg	aac	agg	3090
321	Phe	Gly	Tyr	Asp	Lys	Asp	Thr	Ser	Leu	Leu	Lys	Glu	Ile	Arg	Asn	Arg	
322								905				910				915	
324	ttt	gga	aat	gat	ctt	cac	att	tca	aat	aag	ctg	ttt	gtt	ctg	gat	gtc	3138
325	Phe	Gly	Asn	Asp	Leu	His	Ile	Ser	Asn	Lys	Leu	Phe	Val	Leu	Asp	Ala	
326								920				925				930	
328	ggg	gct	tct	ggg	tca	aag	gac	atg	aag	gta	ctt	cga	aat	cat	ctg	caa	3186
329	Gly	Ala	Ser	Gly	Ser	Lys	Asp	Met	Lys	Val	Leu	Arg	Asn	His	Leu	Gln	
330								935				940				945	
332	gaa	ata	cga	agc	cag	att	gtt	tcg	gtc	tgt	cct	ccc	atg	act	cac	ctg	3234
333	Glu	Ile	Arg	Ser	Gln	Ile	Val	Ser	Val	Cys	Pro	Pro	Met	Thr	His	Leu	

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002  
TIME: 17:06:01

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02052002\J045400.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:39 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3